**Table S3** Nucleotide substitution saturation test on the 291 nuclear protein-coding genes.The nucleotide substitution saturation test calculates an index of substitution saturation (Iss), which is compared to a critical value computed for a symmetrical (Iss.cSym) or extremely asymmetrical (Iss.c asym) tree topology. Pinv: proportion of invariant sites. Iss: index of substitution saturation. Iss.c sym: critical value for symmetrical tree topology. Iss.c asym: critical value for extremely asymmetric tree topology. T: T value. DF: degrees of freedom. P: probability that Iss is significantly different from the critical value (Iss.c sym or Iss.c asym). Two-tailed tests were used.

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